SEQUENCE LISTING

<110> Glucksman, Maria Alexandra
      Williamson, Mark

<120> 22438, 23553, 25278, and 26212 Novel
    Human Sulfatases

<130> 35800/191890(5800-79

<140> 09/495,823
<141> 2000-01-31

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 525
<212> PRT
<213> homo sapiens

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Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys Thr Arg
                20   25   30
Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met Gly Trp
            35   40   45
Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu
        50   55   60
Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala
65   70   75   80
Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu
                85   90   95
Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly
            100   105   110
Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Gln Ala
            115   120   125
Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly
        130   135   140
Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro
145   150   155   160
Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn His Pro
                165   170   175
Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln
            180   185   190
Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn
        195   200   205
Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala
        210   215   220
Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro
225   230   235   240

1

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Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu Pro Val
            245                 250                 255
Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly
            260                 265                 270
Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp
        275                 280                 285
His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly
    290                 295                 300
Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro Phe Thr
305                 310                 315                 320
Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr
            325                 330                 335
Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg
            340                 345                 350
Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu Asp Ile
            355                 360                 365
Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg
    370                 375                 380
Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg Ser Gln
385                 390                 395                 400
Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala Gly Glu
            405                 410                 415
Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr
            420                 425                 430
Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu
            435                 440                 445
Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr Ala Glu
    450                 455                 460
Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro
465                 470                 475                 480
Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala Asn Asp
            485                 490                 495
Asn Ile Ser Ser Ala Asp Tyr Thr Gln Asp Pro Ser Val Thr Pro Cys
            500                 505                 510
Cys Asn Pro Tyr Gln Ile Ala Cys Arg Cys Gln Ala Ala
            515                 520                 525
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<210> 2
<211> 2175
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (248)...(1825)

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tacagccccc aacattccta tagccgttat cactgccatc accactgcca ccagcatctt     120
cttgcagatt ccacccctgc tccccagaga cttcctgctt tgaaagtgag cagaaaggaa     180
gctctcagaa aaatctctag tggtggctgc cgtcgctcca gacaatcgga atcctgcctt     240
caccacc atg ggc tgg ctt ttt cta aag gtt ttg ttg gcg gga gtg agt     289
        Met Gly Trp Leu Phe Leu Lys Val Leu Leu Ala Gly Val Ser
          1               5                  10
```

2

```
ttc tca gga ttt ctt tat cct ctt gtg gat ttt tgc atc agt ggg aaa    337
Phe Ser Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys
 15              20                  25                  30

aca aga gga cag aag cca aac ttt gtg att att ttg gcc gat gac atg    385
Thr Arg Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met
                35                  40                  45

ggg tgg ggt gac ctg gga gca aac tgg gca gaa aca aag gac act gcc    433
Gly Trp Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala
                50                  55                  60

aac ctt gat aag atg gct tcg gag gga atg agg ttt gtg gat ttc cat    481
Asn Leu Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His
             65                  70                  75

gca gct gcc tcc acc tgc tca ccc tcc cgg gct tcc ttg ctc acc ggc    529
Ala Ala Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly
     80                  85                  90

cgg ctt ggc ctt cgc aat gga gtc aca cgc aac ttt gca gtc act tct    577
Arg Leu Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser
 95              100                 105                 110

gtg gga ggc ctt ccg ctc aac gag acc acc ttg gca gag gtg ctg cag    625
Val Gly Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln
                115                 120                 125

cag gcg ggt tac gtc act ggg ata ata ggc aaa tgg cat ctt gga cac    673
Gln Ala Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His
                130                 135                 140

cac ggc tct tat cac ccc aac ttc cgt ggt ttt gat tac tac ttt gga    721
His Gly Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly
                145                 150                 155

atc cca tat agc cat gat atg ggc tgt act gat act cca ggc tac aac    769
Ile Pro Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn
         160                 165                 170

cac cct cct tgt cca gcg tgt cca cag ggt gat gga cca tca agg aac    817
His Pro Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn
175                 180                 185                 190

ctt caa aga gac tgt tac act gac gtg gcc ctc cct ctt tat gaa aac    865
Leu Gln Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn
                195                 200                 205

ctc aac att gtg gag cag ccg gtg aac ttg agc agc ctt gcc cag aag    913
Leu Asn Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys
                210                 215                 220

tat gct gag aaa gca acc cag ttc atc cag cgt gca agc acc agc ggg    961
Tyr Ala Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly
```

3

```
agg ccc ttc ctg ctc tat gtg gct ctg gcc cac atg cac gtg ccc tta    1009
Arg Pro Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu
240                 245                 250

ccc gtg act cag cta cca gca gcg cca cgg ggc aga agc ctg tat ggt    1057
Pro Val Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly
255                 260                 265                 270

gca ggg ctc tgg gag atg gac agt ctg gtg ggc cag atc aag gac aaa    1105
Ala Gly Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys
275                 280                 285

gtt gac cac aca gtg aag gaa aac aca ttc ctc tgg ttt aca gga gac    1153
Val Asp His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp
290                 295                 300

aat ggc ccg tgg gct cag aag tgt gag cta gcg ggc agt gtg ggt ccc    1201
Asn Gly Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro
305                 310                 315

ttc act gga ttt tgg caa act cgt caa ggg gga agt cca gcc aag cag    1249
Phe Thr Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln
320                 325                 330

acg acc tgg gaa gga ggg cac cgg gtc cca gca ctg gct tac tgg cct    1297
Thr Thr Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro
335                 340                 345                 350

ggc aga gtt cca gtt aat gtc acc agc act gcc ttg tta agc gtg ctg    1345
Gly Arg Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu
355                 360                 365

gac att ttt cca act gtg gta gcc ctg gcc cag gcc agc tta cct caa    1393
Asp Ile Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln
370                 375                 380

gga cgg cgc ttt gat ggt gtg gac gtc tcc gag gtg ctc ttt ggc cgg    1441
Gly Arg Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg
385                 390                 395

tca cag cct ggg cac agg gtg ctg ttc cac ccc aac agc ggg gca gct    1489
Ser Gln Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala
400                 405                 410

gga gag ttt gga gcc ctg cag act gtc cgc ctg gag cgt tac aag gcc    1537
Gly Glu Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala
415                 420                 425                 430

ttc tac att acc ggt gga gcc agg gcg tgt gat ggg agc acg ggg cct    1585
Phe Tyr Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro
435                 440                 445

gag ctg cag cat aag ttt cct ctg att ttc aac ctg gaa gac gat acc    1633
Glu Leu Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr
```

4

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Glu Leu Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr
            450             455             460

gca gaa gct gtg ccc cta gaa aga ggt ggt gcg gag tac cag gct gtg    1681
Ala Glu Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val
        465             470             475

ctg ccc gag gtc aga aag gtt ctt gca gac gtc ctc caa gac att gcc    1729
Leu Pro Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala
    480             485             490

aac gac aac atc tcc agc gca gat tac act cag gac cct tca gta act    1777
Asn Asp Asn Ile Ser Ser Ala Asp Tyr Thr Gln Asp Pro Ser Val Thr
495             500             505             510

ccc tgc tgt aat ccc tac caa att gcc tgc cgc tgt caa gcc gca taa    1825
Pro Cys Cys Asn Pro Tyr Gln Ile Ala Cys Arg Cys Gln Ala Ala  *
            515             520             525

cagaccaatt tttattccac gaggaggagt acctggaaat taggcaagtt tgcttccaaa    1885
tttcattttt accctcttta caaacacacg ctttagttta gtcttggagt ttagttttgg    1945
agttagcctt gcatatccct tctgtatcct gtccctcctc cacgccgacc cgagagcagc    2005
tgagctgcgc tggctctggg cagggagtgt gccttaatgg gaagcacacg ggctttggag    2065
tcaggcacag gtgccagctc cagcttttga acttgggcaa ttgtttaacc taacctgcaa    2125
gttgattttg agggttaaat aaaggcatac atgaaaaaaa aaaaaaaaaa               2175


<210> 3
<211> 871
<212> PRT
<213> homo sapiens

<400> 3
Met Lys Tyr Ser Cys Cys Ala Leu Val Leu Ala Val Leu Gly Thr Glu
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Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
        20              25              30
Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
        35              40              45
Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
        50              55              60
Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
65              70              75              80
Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
            85              90              95
Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
            100             105             110
Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
        115             120             125
Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
    130             135             140
Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
145             150             155             160
Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
            165             170             175
Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
```

5

```
                  180                        185                        190
Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
        195                        200                        205
Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
        210                        215                        220
His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225                        230                        235                        240
Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
                  245                        250                        255
Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
                  260                        265                        270
Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
        275                        280                        285
Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
        290                        295                        300
Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305                        310                        315                        320
Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
                  325                        330                        335
Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
                  340                        345                        350
Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
                  355                        360                        365
Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
        370                        375                        380
Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385                        390                        395                        400
Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
                  405                        410                        415
Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
        420                        425                        430
Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
        435                        440                        445
Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
        450                        455                        460
Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465                        470                        475                        480
Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
                  485                        490                        495
Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
                  500                        505                        510
Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
        515                        520                        525
Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
        530                        535                        540
Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
545                        550                        555                        560
Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
                  565                        570                        575
His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
        580         0         585                        590
Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
        595                        600                        605
Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
610                        615                        620
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6

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Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
625                 630                 635                 640
Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
                645                 650                 655
Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
            660                 665                 670
Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
        675                 680                 685
Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
    690                 695                 700
Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
705                 710                 715                 720
Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
                725                 730                 735
Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
            740                 745                 750
His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
            755                 760                 765
Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
    770                 775                 780
Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
785                 790                 795                 800
Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
            805                 810                 815
Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
            820                 825                 830
Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
            835                 840                 845
Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
    850                 855                 860
Leu Trp Asp Gly Trp Glu Gly
865                 870


<210> 4
<211> 4321
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (510)...(3125)

<221> misc_feature
<222> 4310
<223> n = A,T,C or G

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actaggaaac cccaggcgca gaggccagga gcgagggcag cgaggatcag aggccaggcc 120
ttcccggctg ccggcgctcc tcggaggtca gggcagatga ggaacatgac tctccccctt 180
cggaggagga aggaagtccc gctgccacct tatctctgct cctctgcctc ctccctgttc 240
ccagagcttt ttctctagag aagattttga aggcggcttt tgtgctgacg gccacccacc 300
atcatctaaa gaagataaac ttggcaaatg acatgcaggt tcttcaaggc agaataattg 360
cagaaaatct tcaaaggacc ctatctgcag atgttctgaa tacctctgag aatagagatt 420
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7

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gattattcaa ccaggatacc taattcaaga actccagaaa tcaggagacg gagacatttt  480
gtcagttttg caacattgga ccaaataca atg aag tat tct tgc tgt gct ctg     533
                                   Met Lys Tyr Ser Cys Cys Ala Leu
                                   1               5

gtt ttg gct gtc ctg ggc aca gaa ttg ctg gga agc ctc tgt tcg act    581
Val Leu Ala Val Leu Gly Thr Glu Leu Leu Gly Ser Leu Cys Ser Thr
    10              15                  20

gtc aga tcc ccg agg ttc aga gga cgg ata cag cag gaa cga aaa aac    629
Val Arg Ser Pro Arg Phe Arg Gly Arg Ile Gln Gln Glu Arg Lys Asn
    25              30              35                  40

atc cga ccc aac att att ctt gtg ctt acc gat gat caa gat gtg gag    677
Ile Arg Pro Asn Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu
                45                  50                  55

ctg ggg tcc ctg caa gtc atg aac aaa acg aga aag att atg gaa cat    725
Leu Gly Ser Leu Gln Val Met Asn Lys Thr Arg Lys Ile Met Glu His
                60                  65                  70

ggg ggg gcc acc ttc atc aat gcc ttt gtg act aca ccc atg tgc tgc    773
Gly Gly Ala Thr Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys
            75                  80                  85

ccg tca cgg tcc tcc atg ctc acc ggg aag tat gtg cac aat cac aat    821
Pro Ser Arg Ser Ser Met Leu Thr Gly Lys Tyr Val His Asn His Asn
        90                  95                  100

gtc tac acc aac aac gag aac tgc tct tcc ccc tcg tgg cag gcc atg    869
Val Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala Met
105                 110                 115                 120

cat gag cct cgg act ttt gct gta tat ctt aac aac act ggc tac aga    917
His Glu Pro Arg Thr Phe Ala Val Tyr Leu Asn Asn Thr Gly Tyr Arg
                125                 130                 135

aca gcc ttt ttt gga aaa tac ctc aat gaa tat aat ggc agc tac atc    965
Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly Ser Tyr Ile
            140                 145                 150

ccc cct ggg tgg cga gaa tgg ctt gga tta atc aag aat tct cgc ttc   1013
Pro Pro Gly Trp Arg Glu Trp Leu Gly Leu Ile Lys Asn Ser Arg Phe
            155                 160                 165

tat aat tac act gtt tgt cgc aat ggc atc aaa gaa aag cat gga ttt   1061
Tyr Asn Tyr Thr Val Cys Arg Asn Gly Ile Lys Glu Lys His Gly Phe
        170                 175                 180

gat tat gca aag gac tac ttc aca gac tta atc act aac gag agc att   1109
Asp Tyr Ala Lys Asp Tyr Phe Thr Asp Leu Ile Thr Asn Glu Ser Ile
185                 190                 195                 200

aat tac ttc aaa atg tct aag aga atg tat ccc cat agg ccc gtt atg   1157
Asn Tyr Phe Lys Met Ser Lys Arg Met Tyr Pro His Arg Pro Val Met
```

8

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atg gtg atc agc cac gct gcg ccc cac ggc ccc gag gac tca gcc cca   1205
Met Val Ile Ser His Ala Ala Pro His Gly Pro Glu Asp Ser Ala Pro
            220                 225                 230

cag ttt tct aaa ctg tac ccc aat gct tcc caa cac ata act cct agt   1253
Gln Phe Ser Lys Leu Tyr Pro Asn Ala Ser Gln His Ile Thr Pro Ser
            235                 240                 245

tat aac tat gca cca aat atg gat aaa cac tgg att atg cag tac aca   1301
Tyr Asn Tyr Ala Pro Asn Met Asp Lys His Trp Ile Met Gln Tyr Thr
            250                 255                 260

gga cca atg ctg ccc atc cac atg gaa ttt aca aac att cta cag cgc   1349
Gly Pro Met Leu Pro Ile His Met Glu Phe Thr Asn Ile Leu Gln Arg
265                 270                 275                 280

aaa agg ctc cag act ttg atg tca gtg gat gat tct gtg gag agg ctg   1397
Lys Arg Leu Gln Thr Leu Met Ser Val Asp Asp Ser Val Glu Arg Leu
            285                 290                 295

tat aac atg ctc gtg gag acg ggg gag ctg gag aat act tac atc att   1445
Tyr Asn Met Leu Val Glu Thr Gly Glu Leu Glu Asn Thr Tyr Ile Ile
            300                 305                 310

tac acc gcc gac cat ggt tac cat att ggg cag ttt gga ctg gtc aag   1493
Tyr Thr Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly Leu Val Lys
            315                 320                 325

ggg aaa tcc atg cca tat gac ttt gat att cgt gtg cct ttt ttt att   1541
Gly Lys Ser Met Pro Tyr Asp Phe Asp Ile Arg Val Pro Phe Phe Ile
            330                 335                 340

cgt ggt cca agt gta gaa cca gga tca ata gtc cca cag atc gtt ctc   1589
Arg Gly Pro Ser Val Glu Pro Gly Ser Ile Val Pro Gln Ile Val Leu
345                 350                 355                 360

aac att gac ttg gcc ccc acg atc ctg gat att gct ggg ctc gac aca   1637
Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly Leu Asp Thr
            365                 370                 375

cct cct gat gtg gac ggc aag tct gtc ctc aaa ctt ctg gac cca gaa   1685
Pro Pro Asp Val Asp Gly Lys Ser Val Leu Lys Leu Leu Asp Pro Glu
            380                 385                 390

aag cca ggt aac agg ttt cga aca aac aag aag gcc aaa att tgg cgt   1733
Lys Pro Gly Asn Arg Phe Arg Thr Asn Lys Lys Ala Lys Ile Trp Arg
            395                 400                 405

gat aca ttc cta gtg gaa aga ggc aaa ttt cta cgt aag aag gaa gaa   1781
Asp Thr Phe Leu Val Glu Arg Gly Lys Phe Leu Arg Lys Lys Glu Glu
            410                 415                 420

tcc agc aag aat atc caa cag tca aat cac ttg ccc aaa tat gaa cgg   1829
```

Ser Ser Lys Asn Ile Gln Gln Ser Asn His Leu Pro Lys Tyr Glu Arg
425   430   435   440

gtc aaa gaa cta tgc cag cag gcc agg tac cag aca gcc tgt gaa caa   1877
Val Lys Glu Leu Cys Gln Gln Ala Arg Tyr Gln Thr Ala Cys Glu Gln
                445   450   455

ccg ggg cag aag tgg caa tgc att gag gat aca tct ggc aag ctt cga   1925
Pro Gly Gln Lys Trp Gln Cys Ile Glu Asp Thr Ser Gly Lys Leu Arg
                460   465   470

att cac aag tgt aaa gga ccc agt gac ctg ctc aca gtc cgg cag agc   1973
Ile His Lys Cys Lys Gly Pro Ser Asp Leu Leu Thr Val Arg Gln Ser
                475   480   485

acg cgg aac ctc tac gct cgc ggc ttc cat gac aaa gac aaa gag tgc   2021
Thr Arg Asn Leu Tyr Ala Arg Gly Phe His Asp Lys Asp Lys Glu Cys
    490   495   500

agt tgt agg gag tct ggt tac cgt gcc agc aga agc caa aga aag agt   2069
Ser Cys Arg Glu Ser Gly Tyr Arg Ala Ser Arg Ser Gln Arg Lys Ser
505   510   515   520

caa cgg caa ttc ttg aga aac cag ggg act cca aag tac aag ccc aga   2117
Gln Arg Gln Phe Leu Arg Asn Gln Gly Thr Pro Lys Tyr Lys Pro Arg
                525   530   535

ttt gtc cat act cgg cag aca cgt tcc ttg tcc gtc gaa ttt gaa ggt   2165
Phe Val His Thr Arg Gln Thr Arg Ser Leu Ser Val Glu Phe Glu Gly
                540   545   550

gaa ata tat gac ata aat ctg gaa gaa gaa gaa gaa ttg caa gtg ttg   2213
Glu Ile Tyr Asp Ile Asn Leu Glu Glu Glu Glu Glu Leu Gln Val Leu
                555   560   565

caa cca aga aac att gct aag cgt cat gat gaa ggc cac aag ggg cca   2261
Gln Pro Arg Asn Ile Ala Lys Arg His Asp Glu Gly His Lys Gly Pro
    570   575   580

aga gat ctc cag gct tcc agt ggt ggc aac agg ggc agg atg ctg gca   2309
Arg Asp Leu Gln Ala Ser Ser Gly Gly Asn Arg Gly Arg Met Leu Ala
585   590   595   600

gat agc agc aac gcc gtg ggc cca cct acc act gtc cga gtg aca cac   2357
Asp Ser Ser Asn Ala Val Gly Pro Pro Thr Thr Val Arg Val Thr His
                605   610   615

aag tgt ttt att ctt ccc aat gac tct atc cat tgt gag aga gaa ctg   2405
Lys Cys Phe Ile Leu Pro Asn Asp Ser Ile His Cys Glu Arg Glu Leu
                620   625   630

tac caa tcg gcc aga gcg tgg aag gac cat aag gca tac att gac aaa   2453
Tyr Gln Ser Ala Arg Ala Trp Lys Asp His Lys Ala Tyr Ile Asp Lys
                635   640   645

10

```
gag att gaa gct ctg caa gat aaa att aag aat tta aga gaa gtg aga    2501
Glu Ile Glu Ala Leu Gln Asp Lys Ile Lys Asn Leu Arg Glu Val Arg
    650             655             660

gga cat ctg aag aga agg aag cct gag gaa tgt agc tgc agt aaa caa    2549
Gly His Leu Lys Arg Arg Lys Pro Glu Glu Cys Ser Cys Ser Lys Gln
665             670             675             680

agc tat tac aat aaa gag aaa ggt gta aaa aag caa gag aaa tta aag    2597
Ser Tyr Tyr Asn Lys Glu Lys Gly Val Lys Lys Gln Glu Lys Leu Lys
                685             690             695

agc cat ctt cac cca ttc aag gag gct gct cag gaa gta gat agc aaa    2645
Ser His Leu His Pro Phe Lys Glu Ala Ala Gln Glu Val Asp Ser Lys
            700             705             710

ctg caa ctt ttc aag gag aac aac cgt agg agg aag aag gag agg aag    2693
Leu Gln Leu Phe Lys Glu Asn Asn Arg Arg Arg Lys Lys Glu Arg Lys
            715             720             725

gag aag aga cgg cag agg aag ggg gaa gag tgc agc ctg cct ggc ctc    2741
Glu Lys Arg Arg Gln Arg Lys Gly Glu Glu Cys Ser Leu Pro Gly Leu
        730             735             740

act tgc ttc acg cat gac aac aac cac tgg cag aca gcc ccg ttc tgg    2789
Thr Cys Phe Thr His Asp Asn Asn His Trp Gln Thr Ala Pro Phe Trp
745             750             755             760

aac ctg gga tct ttc tgt gct tgc acg agt tct aac aat aac acc tac    2837
Asn Leu Gly Ser Phe Cys Ala Cys Thr Ser Ser Asn Asn Asn Thr Tyr
                765             770             775

tgg tgt ttg cgt aca gtt aat gag acg cat aat ttt ctt ttc tgt gag    2885
Trp Cys Leu Arg Thr Val Asn Glu Thr His Asn Phe Leu Phe Cys Glu
            780             785             790

ttt gct act ggc ttt ttg gag tat ttt gat atg aat aca gat cct tat    2933
Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Met Asn Thr Asp Pro Tyr
            795             800             805

cag ctc aca aat aca gtg cac acg gta gaa cga ggc att ttg aat cag    2981
Gln Leu Thr Asn Thr Val His Thr Val Glu Arg Gly Ile Leu Asn Gln
    810             815             820

cta cac gta caa cta atg gag ctc aga agc tgt caa gga tat aag cag    3029
Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Gln Gly Tyr Lys Gln
825             830             835             840

tgc aac cca aga cct aag aat ctt gat gtt gga aat aaa gat gga gga    3077
Cys Asn Pro Arg Pro Lys Asn Leu Asp Val Gly Asn Lys Asp Gly Gly
                845             850             855

agc tat gac cta cac aga gga cag tta tgg gat gga tgg gaa ggt taa    3125
Ser Tyr Asp Leu His Arg Gly Gln Leu Trp Asp Gly Trp Glu Gly *
            860             865             870
```

11

```
tcagccccgt ctcactgcag acatcaactg gcaaggccta gaggagctac acagtgtgaa 3185
tgaaaacatc tatgagtaca gacaaaacta cagacttagt ctggtggact ggactaatta 3245
cttgaaggat ttagatagag tatttgcact gctgaagagt cactatgagc aaaataaaac 3305
aaataagact caaactgctc aaagtgacgg gttcttggtt gtctctgctg agcacgctgt 3365
gtcaatggag atggcctctg ctgactcaga tgaagaccca aggcataagg ttgggaaaac 3425
acctcatttg accttgccag ctgaccttca aaccctgcat ttgaaccgac caacattaag 3485
tccagagagt aaacttgaat ggaataacga cattccagaa gttaatcatt tgaattctga 3545
acactggaga aaaaccgaaa aatggacggg gcatgaagag actaatcatc tggaaaccga 3605
tttcagtggc gatggcatga cagagctaga gctcgggccc agccccaggc tgcagcccat 3665
tcgcaggcac ccgaaagaac ttccccagta tggtggtcct ggaaaggaca tttttgaaga 3725
tcaactatat cttcctgtgc attccgatgg aatttcagtt catcagatgt tcaccatggc 3785
caccgcagaa caccgaagta attccagcat agcggggaag atgttgacca aggtggagaa 3845
gaatcacgaa aaggagaagt cacagcacct agaaggcagc gcctcctctt cactctcctc 3905
tgattagatg aaactgttac cttaccctaa acacagtatt tcttttaac tttttatt 3965
gtaaactaat aaaggkaatc acagccacca acattccaag ctaccctggg tacctttgtg 4025
cagtagaagc tagtgagcat gtgagcaagc ggtgtgcaca cggagactca tcgttataat 4085
ttactatctg ccaaggagta gaaagaaagg ctggggatat ttgggttggc tttggktttg 4145
attttttgct tggttggttg gtttgkacta aaacagtatt atcttttgaa tatcgtaggg 4205
acataarkww wwwmmwkktw wtcmawymra kakgsywrra wkgggstyty tskkrkstmw 4265
amwykwscmc cyskkrwwaw tywywmmywc mykytssstg rykrnktaat gaagtt 4321
```

<210> 5
<211> 569
<212> PRT
<213> homo sapiens

<400> 5

```
Met His Thr Leu Thr Gly Phe Ser Leu Val Ser Leu Leu Ser Phe Gly
 1               5                  10                  15
Tyr Leu Ser Trp Asp Trp Ala Lys Pro Ser Phe Val Ala Asp Gly Pro
            20                  25                  30
Gly Glu Ala Gly Glu Gln Pro Ser Ala Ala Pro Pro Gln Pro Pro His
            35                  40                  45
Ile Ile Phe Ile Leu Thr Asp Asp Gln Gly Tyr His Asp Val Gly Tyr
     50                  55                  60
His Gly Ser Asp Ile Glu Thr Pro Thr Leu Asp Arg Leu Ala Ala Lys
65                  70                  75                  80
Gly Val Lys Leu Glu Asn Tyr Tyr Ile Gln Pro Ile Cys Thr Pro Ser
                85                  90                  95
Arg Ser Gln Leu Leu Thr Gly Arg Tyr Gln Ile His Thr Gly Leu Gln
            100                 105                 110
His Ser Ile Ile Arg Pro Gln Gln Pro Asn Cys Leu Pro Leu Asp Gln
            115                 120                 125
Val Thr Leu Pro Gln Lys Leu Gln Glu Ala Gly Tyr Ser Thr His Met
    130                 135                 140
Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Leu Pro Thr
145                 150                 155                 160
Arg Arg Gly Phe Asp Thr Phe Leu Gly Ser Leu Thr Gly Asn Val Asp
                165                 170                 175
Tyr Tyr Thr Tyr Asp Asn Cys Asp Gly Pro Gly Val Cys Gly Phe Asp
            180                 185                 190
Leu His Glu Gly Glu Asn Val Ala Trp Gly Leu Ser Gly Gln Tyr Ser
            195                 200                 205
Thr Met Leu Tyr Ala Gln Arg Ala Ser His Ile Leu Ala Ser His Ser
```

12

```
                    210                     215                     220
Pro Gln Arg Pro Leu Phe Leu Tyr Val Ala Phe Gln Ala Val His Thr
225                     230                     235                     240
Pro Leu Gln Ser Pro Arg Glu Tyr Leu Tyr Arg Tyr Arg Thr Met Gly
                    245                     250                     255
Asn Val Ala Arg Arg Lys Tyr Ala Ala Met Val Thr Cys Met Asp Glu
                    260                     265                     270
Ala Val Arg Asn Ile Thr Trp Ala Leu Lys Arg Tyr Gly Phe Tyr Asn
                    275                     280                     285
Asn Ser Val Ile Ile Phe Ser Ser Asp Asn Gly Gly Gln Thr Phe Ser
                    290                     295                     300
Gly Gly Ser Asn Trp Pro Leu Arg Gly Arg Lys Gly Thr Tyr Trp Glu
305                     310                     315                     320
Gly Gly Val Arg Gly Leu Gly Phe Val His Ser Pro Leu Leu Lys Arg
                    325                     330                     335
Lys Gln Arg Thr Ser Arg Ala Leu Met His Ile Thr Asp Trp Tyr Pro
                    340                     345                     350
Thr Leu Val Gly Leu Ala Gly Gly Thr Thr Ser Ala Ala Asp Gly Leu
                    355                     360                     365
Asp Gly Tyr Asp Val Trp Pro Ala Ile Ser Glu Gly Arg Ala Ser Pro
                    370                     375                     380
Arg Thr Glu Ile Leu His Asn Ile Asp Pro Leu Tyr Asn His Ala Gln
385                     390                     395                     400
His Gly Ser Leu Glu Gly Gly Phe Gly Ile Trp Asn Thr Ala Val Gln
                    405                     410                     415
Ala Ala Ile Arg Val Gly Glu Trp Lys Leu Leu Thr Gly Asp Pro Gly
                    420                     425                     430
Tyr Gly Asp Trp Ile Pro Pro Gln Thr Leu Ala Thr Phe Pro Gly Ser
                    435                     440                     445
Trp Trp Asn Leu Glu Arg Met Ala Ser Val Arg Gln Ala Val Trp Leu
                    450                     455                     460
Phe Asn Ile Ser Ala Asp Pro Tyr Glu Arg Glu Asp Leu Ala Gly Gln
465                     470                     475                     480
Arg Pro Asp Val Val Arg Thr Leu Leu Ala Arg Leu Ala Glu Tyr Asn
                    485                     490                     495
Arg Thr Ala Ile Pro Val Arg Tyr Pro Ala Glu Asn Pro Arg Ala His
                    500                     505                     510
Pro Asp Phe Asn Gly Gly Ala Trp Gly Pro Trp Ala Ser Asp Glu Glu
                    515                     520                     525
Glu Glu Glu Glu Glu Gly Arg Ala Arg Ser Phe Ser Arg Gly Arg Arg
                    530                     535                     540
Lys Lys Lys Cys Lys Ile Cys Lys Leu Arg Ser Phe Phe Arg Lys Leu
545                     550                     555                     560
Asn Thr Arg Leu Met Ser Gln Arg Ile
                    565
```

<210> 6
<211> 2940
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (334)...(2043)

13

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ccacgcgtcc gcccacgcgt ccggctgcca cgccgcgtct caggctggcc gggctgagcc       60
ggggaagagg gagcaaaggc ggcgcagggc ctgcgcttag gcagcgggag gcagctcggc      120
gcgggcctga cctccccaga gcgccccgct gcggccgagc agatccggcc cagccgtccg      180
gcagccagtc ccggaccaga cactggaccg tccccggggg gcgctgaact ccctcgcagc      240
atccgagccg gcgggccggt ggtgcgccct gggcgcgcga ggtggtgagg ccccaggagc      300
ccggcgcgcc gggacacgcg ggccggcttg gcg atg cac acc ctc act ggc ttc      354
                                    Met His Thr Leu Thr Gly Phe
                                     1               5
```

```
tct ctg gtc agc ctg ctc agc ttc ggc tac ctg tcc tgg gac tgg gcc       402
Ser Leu Val Ser Leu Leu Ser Phe Gly Tyr Leu Ser Trp Asp Trp Ala
         10                  15                  20
```

```
aag ccg agc ttc gtg gcc gac ggg ccc ggg gag gct ggc gag cag ccc       450
Lys Pro Ser Phe Val Ala Asp Gly Pro Gly Glu Ala Gly Glu Gln Pro
     25                  30                  35
```

```
tcg gcc gct ccg ccc cag cct ccc cac atc atc ttc atc ctc acg gac       498
Ser Ala Ala Pro Pro Gln Pro Pro His Ile Ile Phe Ile Leu Thr Asp
 40                  45                  50                  55
```

```
gac caa ggc tac cac gac gtg ggc tac cat ggt tca gat atc gag acc       546
Asp Gln Gly Tyr His Asp Val Gly Tyr His Gly Ser Asp Ile Glu Thr
                 60                  65                  70
```

```
cct acg ctg gac agg ctg gcg gcc aag ggg gtc aag ttg gag aat tat       594
Pro Thr Leu Asp Arg Leu Ala Ala Lys Gly Val Lys Leu Glu Asn Tyr
                 75                  80                  85
```

```
tac atc cag ccc atc tgc acg cct tcg cgg agc cag ctc ctc act ggc       642
Tyr Ile Gln Pro Ile Cys Thr Pro Ser Arg Ser Gln Leu Leu Thr Gly
             90                  95                 100
```

```
agg tac cag atc cac aca gga ctc cag cat tcc atc atc cgc cca cag       690
Arg Tyr Gln Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Gln
        105                 110                 115
```

```
cag ccc aac tgc ctg ccc ctg gac cag gtg aca ctg cca cag aag ctg       738
Gln Pro Asn Cys Leu Pro Leu Asp Gln Val Thr Leu Pro Gln Lys Leu
120                 125                 130                 135
```

```
cag gag gca ggt tat tcc acc cat atg gtg ggc aag tgg cac ctg ggc       786
Gln Glu Ala Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly
                140                 145                 150
```

```
ttc tac cgg aag gag tgt ctg ccc acc cgt cgg ggc ttc gac acc ttc       834
Phe Tyr Arg Lys Glu Cys Leu Pro Thr Arg Arg Gly Phe Asp Thr Phe
            155                 160                 165
```

```
ctg ggc tcg ctc acg ggc aat gtg gac tat tac acc tat gac aac tgt       882
Leu Gly Ser Leu Thr Gly Asn Val Asp Tyr Tyr Thr Tyr Asp Asn Cys
            170                 175                 180
```

14

```
gat ggc cca ggc gtg tgc ggc ttc gac ctg cac gag ggt gag aat gtg          930
Asp Gly Pro Gly Val Cys Gly Phe Asp Leu His Glu Gly Glu Asn Val
    185                 190                 195

gcc tgg ggg ctc agc ggc cag tac tcc act atg ctt tac gcc cag cgc          978
Ala Trp Gly Leu Ser Gly Gln Tyr Ser Thr Met Leu Tyr Ala Gln Arg
200                 205                 210                 215

gcc agc cat atc ctg gcc agc cac agc cct cag cgt ccc ctc ttc ctc         1026
Ala Ser His Ile Leu Ala Ser His Ser Pro Gln Arg Pro Leu Phe Leu
                220                 225                 230

tat gtg gcc ttc cag gca gta cac aca ccc ctg cag tcc cct cgt gag         1074
Tyr Val Ala Phe Gln Ala Val His Thr Pro Leu Gln Ser Pro Arg Glu
                235                 240                 245

tac ctg tac cgc tac cgc acc atg ggc aat gtg gcc cgg cgg aag tac         1122
Tyr Leu Tyr Arg Tyr Arg Thr Met Gly Asn Val Ala Arg Arg Lys Tyr
                250                 255                 260

gcg gcc atg gtg acc tgc atg gat gag gct gtg cgc aac atc acc tgg         1170
Ala Ala Met Val Thr Cys Met Asp Glu Ala Val Arg Asn Ile Thr Trp
    265                 270                 275

gcc ctc aag cgc tac ggt ttc tac aac aac agt gtc atc atc ttc tcc         1218
Ala Leu Lys Arg Tyr Gly Phe Tyr Asn Asn Ser Val Ile Ile Phe Ser
280                 285                 290                 295

agt gac aat ggt ggc cag act ttc tcg ggg ggc agc aac tgg ccg ctc         1266
Ser Asp Asn Gly Gly Gln Thr Phe Ser Gly Gly Ser Asn Trp Pro Leu
                300                 305                 310

cga gga cgc aag ggc act tat tgg gaa ggt ggc gtg cgg ggc cta ggc         1314
Arg Gly Arg Lys Gly Thr Tyr Trp Glu Gly Gly Val Arg Gly Leu Gly
                315                 320                 325

ttt gtc cac agt ccc ctg ctc aag cga aag caa cgg aca agc cgg gca         1362
Phe Val His Ser Pro Leu Leu Lys Arg Lys Gln Arg Thr Ser Arg Ala
                330                 335                 340

ctg atg cac atc act gac tgg tac ccg acc ctg gtg ggt ctg gca ggt         1410
Leu Met His Ile Thr Asp Trp Tyr Pro Thr Leu Val Gly Leu Ala Gly
                345                 350                 355

ggt acc acc tca gca gcc gat ggg cta gat ggc tac gac gtg tgg ccg         1458
Gly Thr Thr Ser Ala Ala Asp Gly Leu Asp Gly Tyr Asp Val Trp Pro
360                 365                 370                 375

gcc atc agc gag ggc cgg gcc tca cca cgc acg gag atc ctg cac aac         1506
Ala Ile Ser Glu Gly Arg Ala Ser Pro Arg Thr Glu Ile Leu His Asn
                380                 385                 390

att gac cca ctc tac aac cat gcc cag cat ggc tcc ctg gag ggc ggc         1554
Ile Asp Pro Leu Tyr Asn His Ala Gln His Gly Ser Leu Glu Gly Gly
                395                 400                 405
```

15

```
ttt ggc atc tgg aac acc gcc gtg cag gct gcc atc cgc gtg ggt gag     1602
Phe Gly Ile Trp Asn Thr Ala Val Gln Ala Ala Ile Arg Val Gly Glu
        410             415             420

tgg aag ctg ctg aca gga gac ccc ggc tat ggc gat tgg atc cca ccg     1650
Trp Lys Leu Leu Thr Gly Asp Pro Gly Tyr Gly Asp Trp Ile Pro Pro
        425             430             435

cag aca ctg gcc acc ttc ccg ggt agc tgg/tgg aac ctg gaa cga atg     1698
Gln Thr Leu Ala Thr Phe Pro Gly Ser Trp Trp Asn Leu Glu Arg Met
440             445             450             455

gcc agt gtc cgc cag gcc gtg tgg ctc ttc aac atc agt gct gac cct     1746
Ala Ser Val Arg Gln Ala Val Trp Leu Phe Asn Ile Ser Ala Asp Pro
            460             465             470

tat gaa cgg gag gac ctg gct ggc cag cgg cct gat gtg gtc cgc acc     1794
Tyr Glu Arg Glu Asp Leu Ala Gly Gln Arg Pro Asp Val Val Arg Thr
            475             480             485

ctg ctg gct cgc ctg gcc gaa tat aac cgc aca gcc atc ccg gta cgc     1842
Leu Leu Ala Arg Leu Ala Glu Tyr Asn Arg Thr Ala Ile Pro Val Arg
        490             495             500

tac cca gct gag aac ccc cgg gct cat cct gac ttt aat ggg ggt gct     1890
Tyr Pro Ala Glu Asn Pro Arg Ala His Pro Asp Phe Asn Gly Gly Ala
        505             510             515

tgg ggg ccc tgg gcc agt gat gag gaa gag gag gaa gag gaa ggg agg     1938
Trp Gly Pro Trp Ala Ser Asp Glu Glu Glu Glu Glu Glu Glu Gly Arg
520             525             530             535

gct cga agc ttc tcc cgg ggt cgt cgc aag aaa aaa tgc aag att tgc     1986
Ala Arg Ser Phe Ser Arg Gly Arg Arg Lys Lys Lys Cys Lys Ile Cys
            540             545             550

aag ctt cga tcc ttt ttc cgt aaa ctc aac acc agg cta atg tcc caa     2034
Lys Leu Arg Ser Phe Phe Arg Lys Leu Asn Thr Arg Leu Met Ser Gln
            555             560             565

cgg atc tga tggtggggag ggagaaaact gtcctttaga ggatcttccc            2083
Arg Ile *


cactccggct tggccctgct gtttctcagg gagaagcctg tcacatctcc atctacaggg   2143
agttggaggg tgtagagtcc cttggttgaa cagggtaggg agcctggata ggagtgggtg   2203
ggaataaacc agactgggat gcctgtgtct cagtcctgcc tcctcacgga cttgctctgt   2263
gacctcaggt gacccacatg agcttttagc ctcagtttcc tcatctgtaa aatgagctct   2323
aatgactttg tgactctttg gtgtggccct ggagcctggg gccacggtgg agttcctggc   2383
cggccttgcc acttgacaac tcctttaagg cttccccctt aacacgggat ccctgtggtg   2443
gtgtttggga gttgcctgga ggcaactcca agcctggccc ccagctgaag catggcaatc   2503
tggctgctct ctacagggac ccccaagcgc tgtgggtgga gggcaggggt cggggggggtt   2563
gaccttcttg ggtcttcaca tggcctaggc cagtcctccg gtcagactgg tgtcaggcac   2623
cgtggtgcaa aattcctctt ctggcccctc cagtacccag agaaactggc tgggccatta   2683
```

16

```
actgctgcag caccaagggt ggtagaaaga gctgtgaaga gcccccaaac cagtaccagg    2743
acacctgggt tctcctgtga cctggggcac agttcttgcc ctctaggcct tgatttcccc    2803
acctgcaagt ggggatgcca gccctggctc tgcctccttc atgaggctct ggaagactgg    2863
ccaaggttgt ggaggagctt gtgaacttga ttaaagtgtc gtaacatgga aaaaaaaaa     2923
aaaaaaaaa agggcgg                                                     2940
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<210> 7
<211> 550
<212> PRT
<213> homo sapiens

<400> 7

```
Met Ala Pro Arg Gly Cys Ala Gly His Pro Pro Pro Pro Ser Pro Gln
 1               5                  10                  15
Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu Ala Gly
                20                  25                  30
Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser Trp Gly Gln
            35                  40                  45
Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala Gln Ala Gly Glu
        50                  55                  60
Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln Pro His Leu Ile Phe
65                  70                  75                  80
Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp Val Gly Tyr His Gly Ser
                85                  90                  95
Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu Ala Ala Glu Gly Val Lys
            100                 105                 110
Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys Thr Pro Ser Arg Ser Gln
        115                 120                 125
Phe Ile Thr Gly Lys Tyr Gln Ile His Thr Gly Leu Gln His Ser Ile
        130                 135                 140
Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu
145                 150                 155                 160
Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser Thr His Met Val Gly Lys
                165                 170                 175
Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Met Pro Thr Arg Arg Gly
            180                 185                 190
Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr
        195                 200                 205
His Tyr Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu
        210                 215                 220
Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln
225                 230                 235                 240
Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro Thr
                245                 250                 255
Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln Ala Val His Ser Pro Leu
                260                 265                 270
Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile Ile Asn Ile
        275                 280                 285
Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu Asp Glu Ala Ile
        290                 295                 300
Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly Phe Tyr Asn Asn Ser
305                 310                 315                 320
Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly Gln Pro Thr Ala Gly Gly
                325                 330                 335
Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly Thr Tyr Trp Glu Gly Gly
```

17

```
                340                    345                    350
Ile Arg Ala Val Gly Phe Val His Ser Pro Leu Leu Lys Asn Lys Gly
        355                    360                    365
Thr Val Cys Lys Glu Pro Val His Ile Thr Asp Trp Tyr Pro Thr Leu
        370                    375                    380
Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly
385                    390                    395                    400
Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val
                405                    410                    415
Asp Ile Leu His Asn Ile Asp Pro Ile Tyr Thr Lys Ala Lys Asn Gly
        420                    425                    430
Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn Thr Ala Ile Gln Ser Ala
        435                    440                    445
Ile Arg Val Gln His Trp Lys Leu Leu Thr Gly Asn Pro Gly Tyr Ser
        450                    455                    460
Asp Trp Val Pro Pro Gln Ser Phe Ser Asn Leu Gly Pro Asn Arg Trp
465                    470                    475                    480
His Asn Glu Arg Ile Thr Ser Ser Thr Gly Lys Ser Val Trp Leu Phe
                485                    490                    495
Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val Asp Leu Ser Asn Arg Tyr
                500                    505                    510
Pro Gly Ile Val Lys Lys Leu Leu Arg Arg Leu Ser Gln Phe Asn Lys
        515                    520                    525
Thr Ala Val Pro Val Arg Tyr Pro Pro Lys Asp Pro Arg Ser Asn Pro
        530                    535                    540
Arg Leu Asn Gly Gly Val
545                    550
```

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<210> 8
<211> 2266
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (324)...(1977)

<400> 8
cacgcgtccg cccacgcgtc cgtggagata ttaacttttt tctttttttt tttccttggt 60
ggaagctgct ctagggaggg gggaggagga ggagaaagtg aaatgtgctg gagaagagcg 120
agccctcctt gttcttccgg agtcccatcc attaagccat cacttctgga agattaaagt 180
tgtcggacat ggtgacagct gagaggagag gaggatttct tgccaggtgg agagtcttca 240
ccgtctgttg ggtgcatgtg tgcgcccgca scggcgcggg gcgcgtggtt ctccgcgtgg 300
agtctcacct gggacctgag tga atg gct ccc agg ggc tgt gcg ggg cat ccg 353
                         Met Ala Pro Arg Gly Cys Ala Gly His Pro
                          1               5                   10

cct ccg cct tct cca cag gcc tgt gtc tgt cct gga aag atg cta gca    401
Pro Pro Pro Ser Pro Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala
                 15                  20                  25

atg ggg gcg ctg gca gga ttc tgg atc ctc tgc ctc ctc act tat ggt    449
Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly
                 30                  35                  40
```

18

```
tac ctg tcc tgg ggc cag gcc tta gaa gag gag gaa gaa ggg gcc tta      497
Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu
        45                  50                  55

cta gct caa gct gga gag aaa cta gag ccc agc aca act tcc acc tcc      545
Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser
    60                  65                  70

cag ccc cat ctc att ttc atc cta gcg gat gat cag gga ttt aga gat      593
Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
75                  80                  85                  90

gtg ggt tac cac gga tct gag att aaa aca cct act ctt gac aag ctc      641
Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu
                95                  100                 105

gct gcc gaa gga gtt aaa ctg gag aac tac tat gtc cag cct att tgc      689
Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys
            110                 115                 120

aca cca tcc agg agt cag ttt att act gga aag tat cag ata cac acc      737
Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr
            125                 130                 135

gga ctt caa cat tct atc ata aga cct acc caa ccc aac tgt tta cct      785
Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro
        140                 145                 150

ctg gac aat gcc acc cta cct cag aaa ctg aag gag gtt gga tat tca      833
Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser
155                 160                 165                 170

acg cat atg gtc gga aaa tgg cac ttg ggt ttt tac aga aaa gaa tgc      881
Thr His Met Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys
            175                 180                 185

atg ccc acc aga aga gga ttt gat acc ttt ttt ggt tcc ctt ttg gga      929
Met Pro Thr Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly
            190                 195                 200

agt ggg gat tac tat aca cac tac aaa tgt gac agt cct ggg atg tgt      977
Ser Gly Asp Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys
            205                 210                 215

ggc tat gac ttg tat gaa aac gac aat gct gcc tgg gac tat gac aat      1025
Gly Tyr Asp Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn
    220                 225                 230

ggc ata tac tcc aca cag atg tac act cag aga gta cag caa atc tta      1073
Gly Ile Tyr Ser Thr Gln Met Tyr Thr Gln Arg Val Gln Gln Ile Leu
235                 240                 245                 250

gct tcc cat aac ccc aca aag cct ata ttt tta tat att gcc tat caa      1121
Ala Ser His Asn Pro Thr Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln
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gct gtt cat tca cca ctg caa gct cct ggc agg tat ttc gaa cac tac    1169
Ala Val His Ser Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr
            270                 275                 280

cga tcc att atc aac ata aac agg agg aga tat gct gcc atg ctt tcc    1217
Arg Ser Ile Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser
            285                 290                 295

tgc tta gat gaa gca atc aac aac gtg aca ttg gct cta aag act tat    1265
Cys Leu Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr
    300                 305                 310

ggt ttc tat aac aac agc att atc att tac tct tca gat aat ggt ggc    1313
Gly Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly
315                 320                 325                 330

cag cct acg gca gga ggg agt aac tgg cct ctc aga ggt agc aaa gga    1361
Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly
                335                 340                 345

aca tat tgg gaa gga ggg atc cgg gct gta ggc ttt gtg cat agc cca    1409
Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro
                350                 355                 360

ctt ctg aaa aac aag gga aca gtg tgt aag gaa cct gtg cac atc act    1457
Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Pro Val His Ile Thr
            365                 370                 375

gac tgg tac ccc act ctc att tca ctg gct gaa gga cag att gat gag    1505
Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu
    380                 385                 390

gac att caa cta gat ggc tat gat atc tgg gag acc ata agt gag ggt    1553
Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly
395                 400                 405                 410

ctt cgc tca ccc cga gta gat att ttg cat aac att gac ccc ata tac    1601
Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr
                415                 420                 425

acc aag gca aaa aat ggc tcc tgg gca gca ggc tat ggg atc tgg aac    1649
Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn
            430                 435                 440

act gca atc cag tca gcc atc aga gtg cag cac tgg aaa ttg ctt aca    1697
Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr
            445                 450                 455

gga aat cct ggc tac agc gac tgg gtc ccc cct cag tct ttc agc aac    1745
Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn
    460                 465                 470

ctg gga ccg aac cgg tgg cac aat gaa cgg atc acc tcg tca act ggc    1793
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Leu Gly Pro    Arg Trp His Asn Glu Arg Ile Thr Ser Ser Thr Gly
475            480             485             490

aaa agt gta tgg ctt ttc aac atc aca gcc gac cca tat gag agg gtg   1841
Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val
                495             500             505

gac cta tct aac agg tat cca gga atc gtg aag aag ctc cta cgg agg   1889
Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg
            510             515             520

ctc tca cag ttc aac aaa act gca gtg ccg gtc agg tat ccc ccc aaa   1937
Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys
        525             530             535

gac ccc aga agt aac cct agg ctc aat gga ggg gtc tag g gaccatggta  1987
Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val  *
    540             545             550

tagagaggaa accaagaaaa agaagccaag caaaaatcag gctgagaaaa agcaaaagaa  2047
aagcaaaaaa agaagaagaa acagcagaaa gcagtctcag gttcaacttg ccattcaggt  2107
gttacttgtg dataagcaca aatatttcct gtttggttaa actttaatca gttcttatct  2167
ttcatctgtt tcctaggtaa accagcaaat ttggctcgat aatatcgctg gcctaagcgt  2227
caggcttgtt ttcatgctgt gccacctggt gccgaattc                          2266
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